APPENDIX A

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ALIGN calculates a global alignment of two sequences
 version 2.0 Please cite: Myers and Miller, CABIOS (1989) 4:11-17

IFN-B                                                 166 aa vs.
NO.1                                                  166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
99.4% identity;          Global alignment score: 916

              10        20        30        40        50        60
ifn_b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
       ::::::::::::::: :::::::::::::::::::::::::::::::::::::::::::::::
NO.1   MSYNLLGFLQRSSNFQSQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
              10        20        30        40        50        60

              70        80        90       100       110       120
ifn_b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.1   EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
              70        80        90       100       110       120

             130       140       150       160
ifn_b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       :::::::::::::::::::::::::::::::::::::::::::::::
NO.1   HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
             130       140       150       160


IFN-B                                                 166 aa vs.
NO.2                                                  165 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
97.0% identity;          Global alignment score: 875

              10        20        30        40        50        60
ifn_b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
       :   ::  ::::::::: :::::::::::::::::::::::::::::::::::::::::::::
NO.2   MC-NLSQFLQRSSNFQSQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
              10        20        30        40        50

              70        80        90       100       110       120
ifn_b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.2   EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
           60        70        80        90       100       110

             130       140       150       160
ifn_b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       :::::::::::::::::::::::::::::::::::::::::::::::
NO.2   HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
          120       130       140       150       160


IFN-B                                                 166 aa vs.
NO.3                                                  165 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
96.4% identity;          Global alignment score: 874
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                10        20        30        40        50        60
ifn_b.  MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
        :  .:  :::::::::  :::::::::::::::::::::::::::::::::::::::::::::::
NO.3    MC-DLPQFLQRSSNFQSQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
                10        20        30        40        50

                70        80        90       100       110       120
ifn_b.  EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.3    EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
           60        70        80        90       100       110

               130       140       150       160
ifn_b.  HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
        :::::::::::::::::::::::::::::::::::::::::::::::
NO.3    HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
          120       130       140       150       160


IFN-B                                            166 aa vs.
NO.4                                             165 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
97.0% identity;       Global alignment score: 878

                10        20        30        40        50        60
ifn_b.  MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
        ::  .:  :::::::::  :::::::::::::::::::::::::::::::::::::::::::::::
NO.4    MS-DLPQFLQRSSNFQSQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
                10        20        30        40        50

                70        80        90       100       110       120
ifn_b.  EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.4    EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
           60        70        80        90       100       110

               130       140       150       160
ifn_b.  HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
        :::::::::::::::::::::::::::::::::::::::::::::::
NO.4    HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
          120       130       140       150       160


IFN-B                                            166 aa vs.
NO.5                                             165 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
86.8% identity;       Global alignment score: 740

                10        20        30        40        50
ifn_b.  MSYNLLGFLQRSSNFQCQKLLWQLNG-RLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTI
        ::  .:    . .:  .:: ::..     ::::::::::::::::::::::::::::::::::
NO.5    MS-DLPE-THSLDNRRTLMLLAQMSRISPEYCLKDRMNFDIPEEIKQLQQFQKEDAALTI
                10        20        30        40        50
```

-2-

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      60        70        80        90       100       110
ifn_b. YEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.5   YEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS
       60        70        80        90       100       110


      120       130       140       150       160
ifn_b. LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       ::::::::::::::::::::::::::::::::::::::::::::::::
NO.5   LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
      120       130       140       150       160



IFN-B                                          166 aa vs.
NO.6                                            165 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
97.0% identity;        Global alignment score: 884


        10        20        30        40        50        60
ifn_b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
       :  .: :::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.6   MC-DLPQFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
         10        20        30        40        50


        70        80        90       100       110       120
ifn_b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.6   EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
       60        70        80        90       100       110


        130       140       150       160
ifn_b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       ::::::::::::::::::::::::::::::::::::::::::::::::
NO.6   HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
      120       130       140       150       160



IFN-B                                          166 aa vs.
NO.7                                            166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
88.0% identity;        Global alignment score: 824


        10        20        30        40        50        60
ifn_b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.7   MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
        10        20        30        40        50        60


        70        80        90       100       110       120
ifn_b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
       ::::::::::::::::::::::: . ... ...:.:..:  . . :::::::::::::::::
NO.7   EMLQNIFALFRQDSSSTGWNEDLPDKFCTELYQQLNDLEACVMQELEKEDFTRGKLMSSL
        70        80        90       100       110       120
```

```
              130       140       150       160
ifn_b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       ::::::::::::::::::::::::::::::::::::::::::::::::::
NO.7   HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
              130       140       150       160


IFN-B                                          166 aa vs.
NO.8                                           166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
88.0% identity;        Global alignment score: 827

              10        20        30        40        50        60
ifn_b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.8   MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
              10        20        30        40        50        60

              70        80        90        100       110       120
ifn_b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
       ::::::::::::::::::::: .....  ...:.:.:  . . ::::::::::::::::
NO.8   EMLQNIFALFRQDSSSTGWNEDLLDKFCTELYQQLNDLEACVMQELEKEDFTRGKLMSSL
              70        80        90        100       110       120

              130       140       150       160
ifn_b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       ::::::::::::::::::::::::::::::::::::::::::::::::::
NO.8   HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
              130       140       150       160


IFN-B                                          166 aa vs.
NO.9                                           166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
94.0% identity;        Global alignment score: 857

              10        20        30        40        50        60
ifn_b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.9   MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
              10        20        30        40        50        60

              70        80        90        100       110       120
ifn_b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
       ::::::::::::::::::::::::::::::::::::::::::::::::::  .  :::::::
NO.9   EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLMQEERVGETPRGKLMSSL
              70        80        90        100       110       120

              130       140       150       160
ifn_b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       ::::::::::::::::::::::::::::::::::::::::::::::::::
NO.9   HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
              130       140       150       160
```

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IFN-B                                              166 aa vs.
NO.10                                              166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
93.4% identity;         Global alignment score: 847

              10        20        30        40        50        60
ifn_b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
       :::::::::::::::: ::::::::::::::::: .:...:.  . .:::::::::::
NO.10  MSYNLLGFLQRSSNFQSQKLLWQLNGRLEYCLKDRHDFGFPQEEFDGNQFQKEDAALTIY
              10        20        30        40        50        60

              70        80        90       100       110       120
ifn_b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.10  EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
              70        80        90       100       110       120

             130       140       150       160
ifn_b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       ::::::::::::::::::::::::::::::::::::::::::::::::
NO.10  HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
             130       140       150       160


IFN-B                                              166 aa vs.
NO.11                                              166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
97.0% identity;         Global alignment score: 891

              10        20        30        40        50        60
ifn_b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
       :::::::::::::::: ::::::::::::::::: .:...::::::::::::::::::::::
NO.11  MSYNLLGFLQRSSNFQSQKLLWQLNGRLEYCLKDRHDFGFPEEIKQLQQFQKEDAALTIY
              10        20        30        40        50        60

              70        80        90       100       110       120
ifn_b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.11  EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
              70        80        90       100       110       120

             130       140       150       160
ifn_b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       ::::::::::::::::::::::::::::::::::::::::::::::::
NO.11  HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
             130       140       150       160


IFN-B                                              166 aa vs.
NO.12                                              166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
96.4% identity;         Global alignment score: 882
```

```
                  10        20        30        40        50        60
ifn_b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
       :::::::::::::::::::::::::::::::::::::::::::::.:   .  .:::::::::::
NO.12  MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPQEEFDGNQFQKEDAALTIY
                  10        20        30        40        50        60


                  70        80        90       100       110       120
ifn_b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.12  EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
                  70        80        90       100       110       120


                 130       140       150       160
ifn_b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       ::::::::::::::::::::::::::::::::::::::::::::::::
NO.12  HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
                 130       140       150       160


IFN-B                                              166 aa vs.
NO.13                                              166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
94.0% identity;       Global alignment score: 857


                  10        20        30        40        50        60
ifn_b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
       ::::::::::::::::::::::::::::::::::::  .:..:   .  .:::::::::::
NO.13  MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRHDFGFPQEEFDGNQFQKEDAALTIY
                  10        20        30        40        50        60


                  70        80        90       100       110       120
ifn_b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.13  EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
                  70        80        90       100       110       120


                 130       140       150       160
ifn_b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       ::::::::::::::::::::::::::::::::::::::::::::::::
NO.13  HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
                 130       140       150       160


IFN-B                                              166 aa vs.
NO.14                                              166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
99.4% identity;       Global alignment score: 921


                  10        20        30        40        50        60
ifn_b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
       :::::::::::::::::::::::::::::::::::::.:::::::::::::::::::::::::
NO.14  MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFGIPEEIKQLQQFQKEDAALTIY
                  10        20        30        40        50        60
```

```
                70         80         90        100        110        120
ifn_b.  EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.14   EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
                70         80         90        100        110        120


               130        140        150        160
ifn_b.  HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
        :::::::::::::::::::::::::::::::::::::::::::::::
NO.14   HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
               130        140        150        160



IFN-B                                              166 aa vs.
NO.15                                              166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
99.4% identity;        Global alignment score: 916


                10         20         30         40         50         60
ifn_b.  MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
        :::::::::::::::::::::::::::::::::::::::::::::::: :::::::::::::
NO.15   MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQGQQFQKEDAALTIY
                10         20         30         40         50         60


                70         80         90        100        110        120
ifn_b.  EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.15   EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
                70         80         90        100        110        120


               130        140        150        160
ifn_b.  HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
        :::::::::::::::::::::::::::::::::::::::::::::::
NO.15   HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
               130        140        150        160



IFN-B                                              166 aa vs.
NO.16                                              166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
98.8% identity;        Global alignment score: 911


                10         20         30         40         50         60
ifn_b.  MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
        ::::::::::::::::::::::::::::::::::::::::::.::::::.:::::::::::::
NO.16   MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFGIPEEIKQGQQFQKEDAALTIY
                10         20         30         40         50         60


                70         80         90        100        110        120
ifn_b.  EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.16   EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
                70         80         90        100        110        120
```

```
              130       140       150       160
ifn_b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       ::::::::::::::::::::::::::::::::::::::::::::::::::
NO.16  HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
              130       140       150       160


IFN-B                                           166 aa vs.
NO.17                                           166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
94.0% identity;       Global alignment score: 850

              10        20        30        40        50        60
ifn_b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
       ::::::::::::::: :::::::::::::::::: .: ::.:  . .::::::::::::
NO.17  MSYNLLGFLQRSSNFQSQKLLWQLNGRLEYCLKDRHDFRIPQEEFDGNQFQKEDAALTIY
              10        20        30        40        50        60

              70        80        90        100       110       120
ifn_b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.17  EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
              70        80        90        100       110       120

              130       140       150       160
ifn_b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       ::::::::::::::::::::::::::::::::::::::::::::::::::
NO.17  HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
              130       140       150       160


IFN-B                                           166 aa vs.
NO.18                                           166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
93.4% identity;       Global alignment score: 847

              10        20        30        40        50        60
ifn_b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
       :::::::::::::: ::::::::::::::::::. :...:  . .:::::::::::
NO.18  MSYNLLGFLQRSSNFQSQKLLWQLNGRLEYCLKDRKYFGFPQEEFDGNQFQKEDAALTIY
              10        20        30        40        50        60

              70        80        90        100       110       120
ifn_b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.18  EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
              70        80        90        100       110       120

              130       140       150       160
ifn_b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       ::::::::::::::::::::::::::::::::::::::::::::::::::
NO.18  HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
              130       140       150       160
```

```
IFN-B                                            166 aa vs.
NO.19                                            166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
93.4% identity;        Global alignment score: 844

             10        20        30        40        50        60
ifn_b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
       ::::::::::::::::: :::::::::::::::::: .:...: :  . .:::::::::::
NO.19  MSYNLLGFLQRSSNFQSQKLLWQLNGRLEYCLKDRHDFGFPGEEFDGNQFQKEDAALTIY
             10        20        30        40        50        60


             70        80        90       100       110       120
ifn_b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.19  EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
             70        80        90       100       110       120


            130       140       150       160
ifn_b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       ::::::::::::::::::::::::::::::::::::::::::::::::
NO.19  HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
            130       140       150       160



IFN-B                                            166 aa vs.
NO.20                                            166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
94.0% identity;        Global alignment score: 860

             10        20        30        40        50        60
ifn_b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
       :::::::::::::::::::::::::::::::::::: .:...:  . .:::::::::::
NO.20  MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRHDFEFPQEEFDDKQFQKEDAALTIY
             10        20        30        40        50        60


             70        80        90       100       110       120
ifn_b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.20  EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
             70        80        90       100       110       120


            130       140       150       160
ifn_b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       ::::::::::::::::::::::::::::::::::::::::::::::::
NO.20  HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
            130       140       150       160



IFN-B                                            166 aa vs.
NO.21                                            165 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
94.0% identity;        Global alignment score: 851
```

```
            10        20        30        40        50        60
ifn_b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
       ::::::::::::::: ::::::::::::::::: .: :: :. . .:::::::::::
NO.21  MSYNLLGFLQRSSNFQSQKLLWQLNGRLEYCLKDRADFKIPMEMTE-KQFQKEDAALTIY
            10        20        30        40        50

            70        80        90       100       110       120
ifn_b. EMLQNIFALFRQDSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.21  EMLQNIFALFRQDSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
          60        70        80        90       100       110

           130       140       150       160
ifn_b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       ::::::::::::::::::::::::::::::::::::::::::::::::
NO.21  HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
         120       130       140       150       160


IFN-B                                           166 aa vs.
NO.22                                           166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
80.2% identity;       Global alignment score: 680

            10        20        30        40        50
ifn_b. MSYNLLGFLQRSSNFQCQKLLWQLNG-RLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTI
       ::::::::: . .: . .:: :..     ::.:: .:..:.: . .:::. : :::
NO.22  MSYNLLGF-HSLDNRRTLMLLAQMSRISPSSCLMDRHDFGFPQEEFDGNQFQKAPAILTI
            10        20        30        40        50

          60        70        80        90       100       110
ifn_b. YEMLQNIFALFRQDSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.22  YEMLQNIFALFRQDSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS
          60        70        80        90       100       110

          120       130       140       150       160
ifn_b. LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       :::::::::::::::::::::::::::::::::::::::::::::::::
NO.22  LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
         120       130       140       150       160


IFN-B                                           166 aa vs.
NO.23                                           166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
94.6% identity;       Global alignment score: 859

            10        20        30        40        50        60
ifn_b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
       :::::::::::::: ::::::::::::::::::::::::::::  .  .:::. : ::::
NO.23  MSYNLLGFLQRSSNFQSQKLLWQLNGRLEYCLKDRMNFDIPEEEFDGNQFQKAPAILTIY
            10        20        30        40        50        60
```

```
                70        80        90       100       110       120
ifn_b  EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.23  EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
                70        80        90       100       110       120


               130       140       150       160
ifn_b  HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       :::::::::::::::::::::::::::::::::::::::::::::::
NO.23  HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
               130       140       150       160



IFN-B                                        166 aa vs.
NO.24                                        166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
94.0% identity;         Global alignment score: 856


            10        20        30        40        50        60
ifn_b  MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
       :::::::::::::::: :::::::::::::::::::::::::.: . .:::. : ::::
NO.24  MSYNLLGFLQRSSNFQSQKLLWQLNGRLEYCLKDRMNFDIPQEEFDGNQFQKAPAILTIY
            10        20        30        40        50        60


                70        80        90       100       110       120
ifn_b  EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.24  EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
                70        80        90       100       110       120


               130       140       150       160
ifn_b  HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       :::::::::::::::::::::::::::::::::::::::::::::::
NO.24  HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
               130       140       150       160



IFN-B                                        166 aa vs.
NO.25                                        165 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
77.2% identity;         Global alignment score: 638


            10        20        30        40        50
ifn_b  MSYNLLGFLQRSSNFQCQKLLWQLNG-RLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTI
       : .: : . .: . .: :..      ::.:: .:..:.: . .:::. : :::
NO.25  MC-DLPQF-HSLDNRRTLMLLAQMSRISPSSCLMDRHDFGFPQEEFDGNQFQKAPAILTI
               10        20        30        40        50


     60        70        80        90       100       110
ifn_b  YEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.25  YEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS
     60        70        80        90       100       110
```

```
     120        130        140        150        160
ifn_b. LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       :::::::::::::::::::::::::::::::::::::::::::::::::
NO.25  LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
     120        130        140        150        160


IFN-B                                              166 aa vs.
NO.26                                              166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
91.7% identity;        Global alignment score: 812

           10        20        30        40        50
ifn_b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEI--KQLQQFQKEDAALT
       :::::::::::::::: ::::::::: ::::: .:..:.:   .:::::::::::
NO.26  MSYNLLGFLQRSSNFQSQKLLWQLNGR--SCLKDRHDFGFPQEEFDGNLQQFQKEDAALT
           10        20        30        40        50

      60        70        80        90        100       110
ifn_b. IYEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMS
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.26  IYEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMS
      60        70        80        90        100       110

     120        130        140        150        160
ifn_b. SLHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       ::::::::::::::::::::::::::::::::::::::::::::::::::
NO.26  SLHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
     120        130        140        150        160


IFN-B                                              166 aa vs.
NO.27                                              166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
80.2% identity;        Global alignment score: 680

           10        20        30        40        50
ifn_b. MSYNLLGFLQRSSNFQCQKLLWQLNG-RLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTI
       ::::::::: ..   : .:: :..    :::: .:...:  . .::::. : ::
NO.27  MSYNLLGFHSLDNRRTC-MLLAQMSRISPSSCLMDRHDFGFPQEEFDGNQFQKAPAILTI
           10        20        30        40        50

      60        70        80        90        100       110
ifn_b. YEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.27  YEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS
      60        70        80        90        100       110

     120        130        140        150        160
ifn_b. LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       ::::::::::::::::::::::::::::::::::::::::::::::::
NO.27  LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
     120        130        140        150        160
```

```
IFN-B                                                  166 aa vs.
NO.28                                                  166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
85.0% identity;          Global alignment score: 737

               10        20        30        40        50
ifn_b. MSYNLLGFLQRSSNFQCQKLLWQLNG-RLEYCLKDRMNFDIPEEIKLQQFQKEDAALTI
       :::::::::  .  .:  .  .:: :..    ::..:  .:..:.::::::::::::::::
NO.28  MSYNLLGF-HSLDNRRTLMLLAQMSRISPSSCLMDRHDFGFPQEIKLQQFQKEDAALTI
               10        20        30        40        50

      60        70        80        90        100       110
ifn_b. YEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.28  YEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS
      60        70        80        90        100       110

     120       130       140       150       160
ifn_b. LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       :::::::::::::::::::::::::::::::::::::::::::::::::
NO.28  LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
     120       130       140       150       160


IFN-B                                                  166 aa vs.
NO.29                                                  166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
89.8% identity;          Global alignment score: 795

               10        20        30        40        50        60
ifn_b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKLQQFQKEDAALTIY
       :::::::::::::: :::     ::..: .:..:.::::::::::::::::::::::::::
NO.29  MSYNLLGFLQRSSNFQSQKLAQMSRISPSSCLMDRHDFGFPQEIKLQQFQKEDAALTIY
               10        20        30        40        50        60

      70        80        90        100       110       120
ifn_b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.29  EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
      70        80        90        100       110       120

     130       140       150       160
ifn_b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       ::::::::::::::::::::::::::::::::::::::::::::::::
NO.29  HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
     130       140       150       160


IFN-B                                                  166 aa vs.
NO.30                                                  166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
95.2% identity;          Global alignment score: 869
```

```
                10        20        30        40        50        60
ifn_b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
       ::::::::::::::::::::::::::::::::::::::::::  . .:::. : ::::
NO.30  MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEEFDGNQFQKAPAILTIY
                10        20        30        40        50        60

                70        80        90       100       110       120
ifn_b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.30  EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
                70        80        90       100       110       120

               130       140       150       160
ifn_b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       ::::::::::::::::::::::::::::::::::::::::::::::::
NO.30  HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
               130       140       150       160


IFN-B                                          166 aa vs.
NO.31                                          165 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
81.4% identity;        Global alignment score: 683


                10        20        30        40        50
ifn_b. MSYNLLGFLQRSSNFQCQKLLWQL-NGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTI
       :::::::::   .:  : .:: :.. : ::::: .:..:.  .::::... :::
NO.31  MSYNLLGFHSLGSRRTC-MLLAQMRKISLFSCLKDRHDFGFPQEEFG-NQFQKAETILTI
                10        20        30        40        50

       60        70        80        90       100       110
ifn_b. YEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.31  YEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS
       60        70        80        90       100       110

       120       130       140       150       160
ifn_b. LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       :::::::::::::::::::::::::::::::::::::::::::::::::
NO.31  LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       120       130       140       150       160


IFN-B                                          166 aa vs.
NO.32                                          164 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
77.8% identity;        Global alignment score: 629


                10        20        30        40        50
ifn_b. MSYNLLGFLQRSSNFQCQKLLWQL-NGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTI
       :  .:     .:  : .:: :.. : ::::: .:..:.  .::::... :::
NO.32  MC-DLPQTHSLGSRRTC-MLLAQMRKISLFSCLKDRHDFGFPQEEFG-NQFQKAETILTI
                10        20        30        40        50
```

```
        60          70          80          90         100         110
ifn_b.  YEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
NO.32   YEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS
        60          70          80          90         100         110


       120         130         140         150         160
ifn_b.  LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
        :::::::::::::::::::::::::::::::::::::::::::::::::
NO.32   LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
        120         130         140         150         160
```